REMARKS

The above amendments to the above-captioned application along with the following remarks are being submitted as a full and complete response to the Official Action dated March 22, 2004. In view of the above amendments and the following remarks, the Examiner is respectfully requested to give due consideration to this application, to indicate the allowability of the claims, and to pass this case to issue.

Status of the Claims

Claims 1-15 are under consideration in this application. Claims 1-12 are being amended, as set forth in the above marked-up presentation of the claim amendments, in order to more particularly define and distinctly claim applicants' invention. New claims 13-15 are being added to recited another embodiments described in the specification.

Additional Amendments

The claims are being amended to correct formal errors and/or to better recite or describe the features of the present invention as claimed. All the amendments to the claims are supported by the specification. Applicants hereby submit that no new matter is being introduced into the application through the submission of this response.

Formality Rejections

Claim 10 was rejected under 35 U.S.C. § 101 due to the recitation of a use without providing the steps in the process. Claims 1-12 were rejected under 35 U.S.C. § 112, second paragraph, as being vague and indefinite. Claims 1-12 were rejected under 35 U.S.C. § 112, first paragraph, for claiming an invention which is not described in the specification in a manner that will enable a skilled person in the art to make or use the invention. Specifically, the Examiner contended that there was no guidance, direction or examples disclosed in the specification which described the step of "determining whether the second nucleic acid base sequence searched in said step and the first nucleic acid base sequence can be assembled" as recited in the claims.

The method for assembling nucleic acid base sequences of the invention, as now recited in claim 1 (e.g., Fig. 5), comprises the steps of: providing a plurality of nucleic acid base sequences; moving a window 105 of a fixed length along a first nucleic acid base sequence 104

of the plurality of nucleic acid base sequences to define a first fixed-length partial sequence 501 and simultaneously searching for a second nucleic acid base sequence 502 among the plurality of nucleic acid base sequences which has a second fixed-length partial sequence at a terminal region thereof exactly matching (e.g., p. 30, line 18) with the first fixed-length partial sequence 501 defined by the window 105; determining whether the second nucleic acid base sequence 502 searched in said moving step and the first nucleic acid base sequence 104 can be assembled or not by comparing a sequence (~ 503 minus 501 on 104) adjacent to said first fixed-length partial sequence 501 of said first nucleic acid base sequence 104 with a sequence (~ 503 minus 501 on 502) adjacent to said second fixed-length partial sequence of the second nucleic acid base sequence 502 (recited in the original claim 3) to be ***sufficiently similar*** (p. 16, lines 2-3) via a greedy alignment algorithm (Zhang's article1 incorporated by reference on p. 16, lines 8-9); and assembling said first nucleic acid base sequence and said second nucleic acid bases sequence if the second nucleic acid base sequence and the first nucleic acid base sequence are determined to be assembled.

The invention is also directed to a method recited in claim 3 which further introduces a table (Fig. 4; p. 14, lines 12-15) by entering identification information of each of the plurality of nucleic acid base sequences and a respective fixed-length partial sequence located in a terminal region of each of the nucleic acid base sequences thereinto.

The invention is also directed to a method recited in claim 5 (Fig. 2; p.p. 13-16) which further introduces a step of sorting a plurality of nucleic acid base sequences in descending order of sequence lengths, a step of selecting one of the nucleic acid base sequences with longest sequence length as the first consensus sequence, repeating the fourth step to the sixth step are until said fixed length window completes the scanning throughout said first consensus sequence, and repeating said third step to said sixth step until all of the plurality of nucleic acid base sequences are selected in the fourth step and compared in the fifth step.

Claim 9 recites a step of specifying an upper limit c as an expected number of entries retrieved from said table of an identical fixed-length partial sequence located in different nucleic acid base sequences or different positions in the nucleic acid base to be assembled to said first consensus sequences ("*The user can input and specify an upper limit c of an expected value of the number of entries which are found coincidentally despite lack of the true overlap at the time*

1 Zheng Zhang, Scott Schwartz, Lukas Wagner and Webb Miller, "A greedy Algorithm for Aligning DNA Sequences", Journal of Computational Biology, Vol. 7, Numbers ½, 2000, pp. 203-214.

of referring the fixed-length partial sequence table 103 into the inputting and displaying area 1008 in the part 1022 for setting the fixed-length partial sequence length." p. 28, lines 1-6). Claim 12 recites that only entries in said table corresponding to a key, which is the *frequency of occurrence* (p. 14, last paragraph) of said second fixed-length partial sequence in said table, are utilized as said second fixed-length partial sequence for searching for said second nucleic acid base sequence.

As explained on p. 206, third paragraph of Zhang's article (submitted via IDS), "*Greedy alignment algorithms work directly with a measurement of the difference between two sequences, rather than their similarity. In other words, near-identity of sequences is characterized by a small positive number instead of a large one. In the simplest approach, an alignment is assessed by counting the number of its differences, i.e., the number of columns that do not align identical nucleotides. The distance, D(i, j), between the strings a1a2 . . . ai and b1b2 . . . b j is then defined as the minimum number of differences in any alignments of those strings.*"

Applicants contend the recitation in independent claims 1, 3, 5 in conjunction with Zhang's article allows one skilled in the art to "determining whether the second nucleic acid base sequence 502 searched in said moving step and the first nucleic acid base sequence 104 can be assembled or not." Accordingly, the withdrawal of the outstanding ennoblement rejection is in order, and is therefore respectfully solicited.

The remaining rejections under 35 U.S.C. §101 and 112 should be overcome by the newly introduced claim amendments. Accordingly, the withdrawal of the outstanding informality rejections is in order, and is therefore respectfully solicited.

Conclusion

Favorable reconsideration of this application is respectfully solicited. Should there be any outstanding issues requiring discussion that would further the prosecution and allowance of the

above-captioned application, the Examiner is invited to contact the Applicant's undersigned representative at the address and phone number indicated below.

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